

Figure 1

CACCTCTAGC TCGGAGCGGC GTGTAGCGCC ATG GAG AAG AGC AAC GAG ACC AAC	54
Met Glu Lys Ser Asn Glu Thr Asn	
1 5	
GGC TAC CTT GAC AGC GCT CAG GCG GGG CCT GCG GCC GGG CCC GGA GCT	102
Gly Tyr Leu Asp Ser Ala Gln Ala Gly Pro Ala Ala Gly Pro Gly Ala	
10 15 20	
CCG GGG ACC GCG GCG GGA CGC GCA CGG CGT TGC GCG CGC TTC CTG CGG	150
Pro Gly Thr Ala Ala Gly Arg Ala Arg Arg Cys Ala Arg Phe Leu Arg	
25 30 35 40	
CGC CAA GCG CTG GTG CTG CTC ACC GTG TCC GGG GTG CTG GCG GGC GCG	198
Arg Gln Ala Leu Val Leu Leu Thr Val Ser Gly Val Leu Ala Gly Ala	
45 50 55	
GGC CTG GGC GCG GCG TTG CGC GGG CTC AGC CTG AGC CGC ACG CAG GTC	246
Gly Leu Gly Ala Ala Leu Arg Gly Leu Ser Leu Ser Arg Thr Gln Val	
60 65 70	
ACC TAC CTG GCC TTC CCC GGC GAG ATG CTG CTC CGC ATG CTG CGC ATG	294
Thr Tyr Leu Ala Phe Pro Gly Glu Met Leu Leu Arg Met Leu Arg Met	
75 80 85	
ATC ATC CTG CCG CTG GTG GTC TGC AGC CTG GTG TCG GGC GCC GCC TCG	342
Ile Ile Leu Pro Leu Val Val Cys Ser Leu Val Ser Gly Ala Ala Ser	
90 95 100	
CTC GAT GCC AGC TGC CTC GGG CGT CTG GGC GGC ATC CGT GTC GCC TAC	390
Leu Asp Ala Ser Cys Leu Gly Arg Leu Gly Gly Ile Arg Val Ala Tyr	
105 110 115 120	
TTT GGC CTC ACC ACA CTG AGT GCC TCG GCG CTC GCC GTG GCC TTG GCG	438
Phe Gly Leu Thr Thr Leu Ser Ala Ser Ala Leu Ala Val Ala Leu Ala	
125 130 135	
TTC ATC ATC AAG CCA GGA TCC GGT GCG CAG ACC CTT CAG TCC AGC GAC	486
Phe Ile Ile Lys Pro Gly Ser Gly Ala Gln Thr Leu Gln Ser Ser Asp	
140 145 150	
CTG GGG CTG GAG GAC TCG GGG CCT CCT CCT GTC CCC AAA GAG ACG GTG	534
Leu Gly Leu Glu Asp Ser Gly Pro Pro Pro Val Pro Lys Glu Thr Val	
155 160 165	
GAC TCT TTC CTC GAC CTG GCC AGA AAC CTG TTT CCC TCC AAT CTT GTG	582
Asp Ser Phe Leu Asp Leu Ala Arg Asn Leu Phe Pro Ser Asn Leu Val	
170 175 180	

Figure 1 (cont'd.)

GTT GCA GCT TTC CGT ACG TAT GCA ACC GAT TAT AAA GTC GTG ACC CAG	630
Val Ala Ala Phe Arg Thr Tyr Ala Thr Asp Tyr Lys Val Val Thr Gln	
185 190 195 200	
AAC AGC AGC TCT GGA AAT GTA ACC CAT GAA AAG ATC CCC ATA GGC ACT	678
Asn Ser Ser Ser Gly Asn Val Thr His Glu Lys Ile Pro Ile Gly Thr	
205 210 215	
GAG ATA GAA GGG ATG AAC ATT TTA GGA TTG GTC CTG TTT GCT CTG GTG	726
Glu Ile Glu Gly Met Asn Ile Leu Gly Leu Val Leu Phe Ala Leu Val	
220 225 230	
TTA GGA GTG GCC TTA AAG AAA CTA GGC TCC GAA GGA GAA GAC CTC ATC	774
Leu Gly Val Ala Leu Lys Lys Leu Gly Ser Glu Gly Glu Asp Leu Ile	
235 240 245	
CGT TTC TTC AAT TCC CTC AAC GAG GCG ACG ATG GTG CTG GTG TCC TGG	822
Arg Phe Phe Asn Ser Leu Asn Glu Ala Thr Met Val Leu Val Ser Trp	
250 255 260	
ATT ATG TGG TAC GTA CCT GTG GGC ATC ATG TTC CTT GTT GGA AGC AAG	870
Ile Met Trp Tyr Val Pro Val Gly Ile Met Phe Leu Val Gly Ser Lys	
265 270 275 280	
ATC GTG GAA ATG AAA GAC ATC ATC GTG CTG GTG ACC AGC CTG GGG AAA	918
Ile Val Glu Met Lys Asp Ile Ile Val Leu Val Thr Ser Leu Gly Lys	
285 290 295	
TAC ATC TTC GCA TCT ATA TTG GGC CAT GTT ATT CAT GGA GGA ATT GTT	966
Tyr Ile Phe Ala Ser Ile Leu Gly His Val Ile His Gly Gly Ile Val	
300 305 310	
CTG CCA CTT ATT TAT TTT GTT TTC ACA CGA AAA AAC CCA TTC AGA TTC	1014
Leu Pro Leu Ile Tyr Phe Val Phe Thr Arg Lys Asn Pro Phe Arg Phe	
315 320 325	
CTC CTG GGC CTC CTC GCC CCA TTT GCG ACA GCA TTT GCT ACC TGC TCC	1062
Leu Leu Gly Leu Leu Ala Pro Phe Ala Thr Ala Phe Ala Thr Cys Ser	
330 335 340	
AGC TCA GCG ACC CTT CCC TCT ATG ATG AAG TGC ATT GAA GAG AAC AAT	1110
Ser Ser Ala Thr Leu Pro Ser Met Met Lys Cys Ile Glu Glu Asn Asn	
345 350 355 360	
GGT GTG GAC AAG AGG ATC AGC AGG TTT ATT CTC CCC ATC GGG GCC ACC	1158
Gly Val Asp Lys Arg Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr	
365 370 375	
GTG AAC ATG GAC GGA GCA GCC ATC TTC CAG TGT GTG GCC GCG GTG TTC	1206
Val Asn Met Asp Gly Ala Ala Ile Phe Gln Cys Val Ala Ala Val Phe	
380 385 390	

Figure 1 (cont'd.)

ATT GCG CAA CTC AAC AAC ATA GAG CTC AAC GCA GGA CAG ATT TTC ACC Ile Ala Gln Leu Asn Asn Ile Glu Leu Asn Ala Gly Gln Ile Phe Thr 395 400 405	1254
ATT CTA GTG ACT GCC ACA GCG TCC AGT GTT GGA GCA GCA GGC GTG CCA Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Val Pro 410 415 420	1302
GCT GGA GGG GTC CTC ACC ATT GCC ATT ATC CTG GAG GCC ATT GGG CTG Ala Gly Gly Val Leu Thr Ile Ala Ile Ile Leu Glu Ala Ile Gly Leu 425 430 435 440	1350
CCT ACT CAT GAC CTG CCT CTG ATC CTG GCT GTG GAC TGG ATT GTG GAC Pro Thr His Asp Leu Pro Leu Ile Leu Ala Val Asp Trp Ile Val Asp 445 450 455	1398
CGG ACC ACC ACG GTG GTG AAT GTG GAG GGG GAT GCC CTG GGT GCA GGC Arg Thr Thr Thr Val Val Asn Val Glu Gly Asp Ala Leu Gly Ala Gly 460 465 470	1446
ATT CTC CAC CAC CTG AAT CAG AAG GCA ACA AAG AAA GGC GAG CAG GAA Ile Leu His His Leu Asn Gln Lys Ala Thr Lys Lys Gly Glu Gln Glu 475 480 485	1494
CTT GCT GAG GTG AAA GTG GAA GCC ATC CCC AAC TGC AAG TCT GAG GAG Leu Ala Glu Val Lys Val Glu Ala Ile Pro Asn Cys Lys Ser Glu Glu 490 495 500	1542
GAG ACA TCG CCC CTG GTG ACA CAC CAG AAC CCC GCT GGC CCC GTG GCC Glu Thr Ser Pro Leu Val Thr His Gln Asn Pro Ala Gly Pro Val Ala 505 510 515 520	1590
AGT GCC CCA GAA CTG GAA TCC AAG GAG TCG GTT CTG TGATGGGGCT Ser Ala Pro Glu Leu Glu Ser Lys Glu Ser Val Leu 525 530	1636
GGGCTTTGGG CTTGCCTGCC AGCAGTGATG TCCCACCCTG TTCA	1680

Figure 2

AAAGAAGAGA CCCTCCTAGA AAAGTAAAT ATG ACT AAA AGC AAT GGA GAA GAG	54
Met Thr Lys Ser Asn Gly Glu Glu	
1 5	
CCC AAG ATG GGG GGC AGG ATG GAG AGA TTC CAG CAG GGA GTC CGT AAA	102
Pro Lys Met Gly Gly Arg Met Glu Arg Phe Gln Gln Gly Val Arg Lys	
10 15 20	
CGC ACA CTT TTG GCC AAG AAG AAA GTG CAG AAC ATT ACA AAG GAG GTT	150
Arg Thr Leu Leu Ala Lys Lys Lys Val Gln Asn Ile Thr Lys Glu Val	
25 30 35 40	
GTT AAA AGT TAC CTG TTT CGG AAT GCT TTT GTG CTG CTC ACA GTC ACC	198
Val Lys Ser Tyr Leu Phe Arg Asn Ala Phe Val Leu Leu Thr Val Thr	
45 50 55	
GCT GTC ATT GTG GGT ACA ATC CTT GGA TTT ACC CTC CGA CCA TAC AGA	246
Ala Val Ile Val Gly Thr Ile Leu Gly Phe Thr Leu Arg Pro Tyr Arg	
60 65 70	
ATG AGC TAC CGG GAA GTC AAG TAC TTC TCC TTT CCT GGG GAA CTT CTG	294
Met Ser Tyr Arg Glu Val Lys Tyr Phe Ser Phe Pro Gly Glu Leu Leu	
75 80 85	
ATG AGG ATG TTA CAG ATG CTG GTC TTA CCA CTT ATC ATC TCC AGT CTT	342
Met Arg Met Leu Gln Met Leu Val Leu Pro Leu Ile Ile Ser Ser Leu	
90 95 100	
GTC ACA GGA ATG GCG GCG CTA GAT AGT AAG GCA TCA GGG AAG TGG GAA	390
Val Thr Gly Met Ala Ala Leu Asp Ser Lys Ala Ser Gly Lys Trp Glu	
105 110 115 120	
TGC GGA GCT GTA GTC TAT TAT ATG ACT ACC ACC ATC ATT GCT GTG GTG	438
Cys Gly Ala Val Val Tyr Tyr Met Thr Thr Thr Ile Ile Ala Val Val	
125 130 135	
ATT GGC ATA ATC ATT GTC ATC ATC ATC CAT CCT GGG AAG GGC ACA AAG	486
Ile Gly Ile Ile Ile Val Ile Ile Ile His Pro Gly Lys Gly Thr Lys	
140 145 150	
GAA AAC ATG CAC AGA GAA GGC AAA ATT GTA CGA GTG ACA GCT GCA GAT	534
Glu Asn Met His Arg Glu Gly Lys Ile Val Arg Val Thr Ala Ala Asp	
155 160 165	
GCC TTC CTG GAC TTG ATC AGG AAC ATG TTA AAT CCA AAT CTG GTA GAA	582
Ala Phe Leu Asp Leu Ile Arg Asn Met Leu Asn Pro Asn Leu Val Glu	
170 175 180	
GCC TGC TTT AAA CAG TTT AAA ACC AAC TAT GAG AAG AGA AGC TTT AAA	630
Ala Cys Phe Lys Gln Phe Lys Thr Asn Tyr Glu Lys Arg Ser Phe Lys	
185 190 195 200	

Figure 2 (cont'd.)

GTG CCC ATC CAG GCC AAC GAA ACG CTT GTG GGT GCT GTG ATA AAC AAT	678
Val Pro Ile Gln Ala Asn Glu Thr Leu Val Gly Ala Val Ile Asn Asn	
205 210 215	
GTG TCT GAG GCC ATG GAG ACT CTT ACC CGA ATC ACA GAG GAG CTG GTC	726
Val Ser Glu Ala Met Glu Thr Leu Thr Arg Ile Thr Glu Glu Leu Val	
220 225 230	
CCA GTT CCA GGA TCT GTG AAT GGA GTC AAT GCC CTG GGT CTA GTT GTC	774
Pro Val Pro Gly Ser Val Asn Gly Val Asn Ala Leu Gly Leu Val Val	
235 240 245	
TTC TCC ATG TGC TTC GGT TTT GTG ATT GGA AAC ATG AAG GAA CAG GGG	822
Phe Ser Met Cys Phe Gly Phe Val Ile Gly Asn Met Lys Glu Gln Gly	
250 255 260	
CAG GCC CTG AGA GAG TTC TTT GAT TCT CTT AAC GAA GCC ATC ATG AGA	870
Gln Ala Leu Arg Glu Phe Phe Asp Ser Leu Asn Glu Ala Ile Met Arg	
265 270 275 280	
CTG GTA GCA GTA ATA ATG TGG TAT GCC CCC GTG GGT ATT CTC TTC CTG	918
Leu Val Ala Val Ile Met Trp Tyr Ala Pro Val Gly Ile Leu Phe Leu	
285 290 295	
ATT GCT GGG AAG ATT GTG GAG ATG GAA GAC ATG GGT GTG ATT GGG GGG	966
Ile Ala Gly Lys Ile Val Glu Met Glu Asp Met Gly Val Ile Gly Gly	
300 305 310	
CAG CTT GCC ATG TAC ACC GTG ACT GTC ATT GTT GGC TTA CTC ATT CAC	1014
Gln Leu Ala Met Tyr Thr Val Thr Val Ile Val Gly Leu Leu Ile His	
315 320 325	
GCA GTC ATC GTC TTG CCA CTC CTC TAC TTC TTG GTA ACA CGG AAA AAC	1062
Ala Val Ile Val Leu Pro Leu Leu Tyr Phe Leu Val Thr Arg Lys Asn	
330 335 340	
CCT TGG GTT TTT ATT GGA GGG TTG CTG CAA GCA CTC ATC ACC GCT CTG	1110
Pro Trp Val Phe Ile Gly Gly Leu Leu Gln Ala Leu Ile Thr Ala Leu	
345 350 355 360	
GGG ACC TCT TCA AGT TCT GCC ACC CTA CCC ATC ACC TTC AAG TGC CTG	1158
Gly Thr Ser Ser Ser Ala Thr Leu Pro Ile Thr Phe Lys Cys Leu	
365 370 375	
GAA GAG AAC AAT GGC GTG GAC AAG CGC GTC ACC AGA TTC GTG CTC CCC	1206
Glu Glu Asn Asn Gly Val Asp Lys Arg Val Thr Arg Phe Val Leu Pro	
380 385 390	
GTA GGA GCC ACC ATT AAC ATG GAT GGG ACT GCC CTC TAT GAG GCT TTG	1254
Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Leu	
395 400 405	

Figure 2 (cont'd.)

GCT GCC ATT TTC ATT GCT CAA GTT AAC AAC TTT GAA CTG AAC TTC GGA Ala Ala Ile Phe Ile Ala Gln Val Asn Asn Phe Glu Leu Asn Phe Gly 410 415 420	1302
CAA ATT ATT ACA ATC AGC ATC ACA GCC ACA GCT GCC AGT ATT GGG GCA Gln Ile Ile Thr Ile Ser Ile Thr Ala Thr Ala Ala Ser Ile Gly Ala 425 430 435 440	1350
GCT GGA ATT CCT CAG GCG GGC CTG GTC ACT ATG GTC ATT GTG CTG ACA Ala Gly Ile Pro Gln Ala Gly Leu Val Thr Met Val Ile Val Leu Thr 445 450 455	1398
TCT GTC GGC CTG CCC ACT GAC GAC ATC ACG CTC ATC ATC GCG GTG GAC Ser Val Gly Leu Pro Thr Asp Asp Ile Thr Leu Ile Ile Ala Val Asp 460 465 470	1446
TGG TTC TTG GAT CGC CTC CGG ACC ACC ACC AAC GTA CTG GGA GAC TCC Trp Phe Leu Asp Arg Leu Arg Thr Thr Thr Asn Val Leu Gly Asp Ser 475 480 485	1494
CTG GGA GCT GGG ATT GTG GAG CAC TTG TCA CGA CAT GAA CTG AAG AAC Leu Gly Ala Gly Ile Val Glu His Leu Ser Arg His Glu Leu Lys Asn 490 495 500	1542
AGA GAT GTT GAA ATG GGT AAC TCA GTG ATT GAA GAG AAT GAA ATG AAG Arg Asp Val Glu Met Gly Asn Ser Val Ile Glu Glu Asn Glu Met Lys 505 510 515 520	1590
AAA CCA TAT CAA CTG ATT GCA CAG GAC AAT GAA ACT GAG AAA CCC ATC Lys Pro Tyr Gln Leu Ile Ala Gln Asp Asn Glu Thr Glu Lys Pro Ile 525 530 535	1638
GAC AGT GAA ACC AAG ATG TAGACTAACA TAAAGAAACA CTTT Asp Ser Glu Thr Lys Met 540	1680

Figure 3

GATAGTGCTG AAGAGGAGGG GCGTTCCCAG ACC ATG GCA TCT ACG GAA GGT GCC	54
Met Ala Ser Thr Glu Gly Ala	
1 5	
AAC AAT ATG CCC AAG CAG GTG GAA GTG CGA ATG CCA GAC AGT CAT CTT	102
Asn Asn Met Pro Lys Gln Val Glu Val Arg Met Pro Asp Ser His Leu	
10 15 20	
GGC TCA GAG GAA CCC AAG CAC CGG CAC CTG GGC CTG CGC CTG TGT GAC	150
Gly Ser Glu Glu Pro Lys His Arg His Leu Gly Leu Arg Leu Cys Asp	
25 30 35	
AAG CTG GGG AAG AAT CTG CTG CTC ACC CTG ACG GTG TTT GGT GTC ATC	198
Lys Leu Gly Lys Asn Leu Leu Leu Thr Leu Thr Val Phe Gly Val Ile	
40 45 50 55	
CTG GGA GCA GTG TGT GGA GGG CTT CTT CGC TTG GCA TCT CCC ATC CAC	246
Leu Gly Ala Val Cys Gly Gly Leu Leu Arg Leu Ala Ser Pro Ile His	
60 65 70	
CCT GAT GTG GTT ATG TTA ATA GCC TTC CCA GGG GAT ATA CTC ATG AGG	294
Pro Asp Val Val Met Leu Ile Ala Phe Pro Gly Asp Ile Leu Met Arg	
75 80 85	
ATG CTA AAA ATG CTC ATT CTG GGT CTA ATC ATC TCC AGC TTA ATC ACA	342
Met Leu Lys Met Leu Ile Leu Gly Leu Ile Ile Ser Ser Leu Ile Thr	
90 95 100	
GGG TTG TCA GGC CTG GAT GCT AAG GCT AGT GGC CGC TTG GGC ACG AGA	390
Gly Leu Ser Gly Leu Asp Ala Lys Ala Ser Gly Arg Leu Gly Thr Arg	
105 110 115	
GCC ATG GTG TAT TAC ATG TCC ACG ACC ATC ATT GCT GCA GTA CTG GGG	438
Ala Met Val Tyr Tyr Met Ser Thr Thr Ile Ile Ala Ala Val Leu Gly	
120 125 130 135	
GTC ATT CTG GTC TTG GCT ATC CAT CCA GGC AAT CCC AAG CTC AAG AAG	486
Val Ile Leu Val Leu Ala Ile His Pro Gly Asn Pro Lys Leu Lys Lys	
140 145 150	
CAG CTG GGG CCT GGG AAG AAG AAT GAT GAA GTG TCC AGC CTG GAT GCC	534
Gln Leu Gly Pro Gly Lys Lys Asn Asp Glu Val Ser Ser Leu Asp Ala	
155 160 165	
TTC CTG GAC CTT ATT CGA AAT CTC TTC CCT GAA AAC CTT GTC CAA GCC	582
Phe Leu Asp Leu Ile Arg Asn Leu Phe Pro Glu Asn Leu Val Gln Ala	
170 175 180	
TGC TTT CAA CAG ATT CAA ACA GTG ACG AAG AAA GTC CTG GTT GCA CCA	630
Cys Phe Gln Gln Ile Gln Thr Val Thr Lys Lys Val Leu Val Ala Pro	
185 190 195	

Figure 3 (cont'd.)

CCG CCA GAC GAG GAG GCC AAC GCA ACC AGC GCT GAA GTC TCT CTG TTG	678
Pro Pro Asp Glu Glu Ala Asn Ala Thr Ser Ala Glu Val Ser Leu Leu	
200 205 210 215	
AAC GAG ACT GTG ACT GAG GTG CCG GAG GAG ACT AAG ATG GTT ATC AAG	726
Asn Glu Thr Val Thr Glu Val Pro Glu Glu Thr Lys Met Val Ile Lys	
220 225 230	
AAG GGC CTG GAG TTC AAG GAT GGG ATG AAC GTC TTA GGT CTG ATA GGG	774
Lys Gly Leu Glu Phe Lys Asp Gly Met Asn Val Leu Gly Leu Ile Gly	
235 240 245	
TTT TTC ATT GCT TTT GGC ATC GCT ATG GGG AAG ATG GGA GAT CAG GCC	822
Phe Phe Ile Ala Phe Gly Ile Ala Met Gly Lys Met Gly Asp Gln Ala	
250 255 260	
AAG CTG ATG GTG GAT TTC TTC AAC ATT TTG AAT GAG ATT GTA ATG AAG	870
Lys Leu Met Val Asp Phe Phe Asn Ile Leu Asn Glu Ile Val Met Lys	
265 270 275	
TTA GTG ATC ATG ATC ATG TGG TAC TCT CCC CTG GGT ATC GCC TGC CTG	918
Leu Val Ile Met Ile Met Trp Tyr Ser Pro Leu Gly Ile Ala Cys Leu	
280 285 290 295	
ATC TGT GGA AAG ATC ATT GCA ATC AAG GAC TTA GAA GTG GTT GCT AGG	966
Ile Cys Gly Lys Ile Ile Ala Ile Lys Asp Leu Glu Val Val Ala Arg	
300 305 310	
CAA CTG GGG ATG TAC ATG GTA ACA GTG ATC ATA GGC CTC ATC ATC CAC	1014
Gln Leu Gly Met Tyr Met Val Thr Val Ile Ile Gly Leu Ile Ile His	
315 320 325	
GGG GGC ATC TTT CTC CCC TTG ATT TAC TTT GTA GTG ACC AGG AAA AAC	1062
Gly Gly Ile Phe Leu Pro Leu Ile Tyr Phe Val Val Thr Arg Lys Asn	
330 335 340	
CCC TTC TCC CTT TTT GCT GGC ATT TTC CAA GCT TGG ATC ACT GCC CTG	1110
Pro Phe Ser Leu Phe Ala Gly Ile Phe Gln Ala Trp Ile Thr Ala Leu	
345 350 355	
GGC ACC GCT TCC AGT GCT GGA ACT TTG CCT GTC ACC TTT CGT TGC CTG	1158
Gly Thr Ala Ser Ser Ala Gly Thr Leu Pro Val Thr Phe Arg Cys Leu	
360 365 370 375	
GAA GAA AAT CTG GGG ATT GAT AAG CGT GTG ACT AGA TTC GTC CTT CCT	1206
Glu Glu Asn Leu Gly Ile Asp Lys Arg Val Thr Arg Phe Val Leu Pro	
380 385 390	
GTT GGA GCA ACC ATT AAC ATG GAT GGT ACA GCC CTT TAT GAA GCG GTG	1254
Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val	
395 400 405	



Figure 3 (cont'd.)

GCC GCC ATC TTT ATA GCC CAA ATG AAT GGT GTT GTC CTG GAT GGA GGA Ala Ala Ile Phe Ile Ala Gln Met Asn Gly Val Val Leu Asp Gly Gly 410 415 420	1302
CAG ATT GTG ACT GTA AGC CTC ACA GCC ACC CTG GCA AGC GTC GGC GCG Gln Ile Val Thr Val Ser Leu Thr Ala Thr Leu Ala Ser Val Gly Ala 425 430 435	1350
GCC AGT ATC CCC AGT GCC GGG CTG GTC ACC ATG CTC CTC ATT CTG ACA Ala Ser Ile Pro Ser Ala Gly Leu Val Thr Met Leu Leu Ile Leu Thr 440 445 450 455	1398
GCC GTG GGC CTG CCA ACA GAG GAC ATC AGC TTG CTG GTG GCT GTG GAC Ala Val Gly Leu Pro Thr Glu Asp Ile Ser Leu Leu Val Ala Val Asp 460 465 470	1446
TGG CTG CTG GAC AGG ATG AGA ACT TCA GTC AAT GTT GTG GGT GAC TCT Trp Leu Leu Asp Arg Met Arg Thr Ser Val Asn Val Val Gly Asp Ser 475 480 485	1494
TTT GGG GCT GGG ATA GTC TAT CAC CTC TCC AAG TCT GAG CTG GAT ACC Phe Gly Ala Gly Ile Val Tyr His Leu Ser Lys Ser Glu Leu Asp Thr 490 495 500	1542
ATT GAC TCC CAG CAT CGA GTG CAT GAA GAT ATT GAA ATG ACC AAG ACT Ile Asp Ser Gln His Arg Val His Glu Asp Ile Glu Met Thr Lys Thr 505 510 515	1590
CAA TCC ATT TAT GAT GAC ATG AAG AAC CAC AGG GAA AGC AAC TCT AAT Gln Ser Ile Tyr Asp Asp Met Lys Asn His Arg Glu Ser Asn Ser Asn 520 525 530 535	1638
CAA TGT GTC TAT GCT GCA CAC AAC TCT GTC ATA GTA GAT GAA TGC AAG Gln Cys Val Tyr Ala Ala His Asn Ser Val Ile Val Asp Glu Cys Lys 540 545 550	1686
GTA ACT CTG GCA GCC AAT GGA AAG TCA GCC GAC TGC AGT GTT GAG GAA Val Thr Leu Ala Ala Asn Gly Lys Ser Ala Asp Cys Ser Val Glu Glu 555 560 565	1734
GAA CCT TGG AAA CGT GAG AAA TAAGGATATG AGTCTCAGCA AATTCTTGAA Glu Pro Trp Lys Arg Glu Lys 570	1785
TAAACTCCCC AGCGT	1800

Figure 4

ATAGCGGCGA CAGCC ATG GGG AAA CCG GCG AGG AAA GGA TGC CCG AGT TGG	51
Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp	
1 5 10	
AAG CGC TTC CTG AAG AAT AAC TGG GTG TTG CTG TCC ACC GTG GCC GCG	99
Lys Arg Phe Leu Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala	
15 20 25	
GTG GTG CTA GGC ATT ACC ACA GGA GTC TTG GTT CGA GAA CAC AGC AAC	147
Val Val Leu Gly Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn	
30 35 40	
CTC TCA ACT CTA GAG AAA TTC TAC TTT GCT TTT CCT GGA GAA ATT CTA	195
Leu Ser Thr Leu Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu	
45 50 55 60	
ATG CGG ATG CTG AAA CTC ATC ATT TTG CCA TTA ATT ATA TCC AGC ATG	243
Met Arg Met Leu Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met	
65 70 75	
ATT ACA GGT GTT GCT GCA CTG GAT TCC AAC GTA TCC GGA AAA ATT GGT	291
Ile Thr Gly Val Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly	
80 85 90	
CTG CGC GCT GTC GTG TAT TAT TTC TGT ACC ACT CTC ATT GCT GTT ATT	339
Leu Arg Ala Val Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile	
95 100 105	
CTA GGT ATT GTG CTG GTG GTG AGC ATC AAG CCT GGT GTC ACC CAG AAA	387
Leu Gly Ile Val Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys	
110 115 120	
GTG GGT GAA ATT GCG AGG ACA GGC AGC ACC CCT GAA GTC AGT ACG GTG	435
Val Gly Glu Ile Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val	
125 130 135 140	
GAT GCC ATG TTA GAT CTC ATC AGG AAT ATG TTC CCT GAG AAT CTT GTC	483
Asp Ala Met Leu Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val	
145 150 155	
CAG GCC TGT TTT CAG CAG TAC AAA ACT AAG CGT GAA GAA GTG AAG CCT	531
Gln Ala Cys Phe Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro	
160 165 170	
CCC AGC GAT CCA GAG ATG AAC ATG ACA GAA GAG TCC TTC ACA GCT GTC	579
Pro Ser Asp Pro Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val	
175 180 185	
ATG ACA ACT GCA ATT TCC AAG AAC AAA ACA AAG GAA TAC AAA ATT GTT	627
Met Thr Thr Ala Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val	
190 195 200	

Figure 4 (cont'd.)

GGC ATG TAT TCA GAT GGC ATA AAC GTC CTG GGC TTG ATT GTC TTT TGC Gly Met Tyr Ser Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys 205 210 215 220	675
CTT GTC TTT GGA CTT GTC ATT GGA AAA ATG GGA GAA AAG GGA CAA ATT Leu Val Phe Gly Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile 225 230 235	723
CTG GTG GAT TTC TTC AAT GCT TTG AGT GAT GCA ACC ATG AAA ATC GTT Leu Val Asp Phe Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val 240 245 250	771
CAG ATC ATC ATG TGT TAT ATG CCA CTA GGT ATT TTG TTC CTG ATT GCT Gln Ile Ile Met Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala 255 260 265	819
GGG AAG ATC ATA GAA GTT GAA GAC TGG GAA ATA TTC CGC AAG CTG GGC Gly Lys Ile Ile Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly 270 275 280	867
CTT TAC ATG GCC ACA GTC CTG ACT GGG CTT GCA ATC CAC TCC ATT GTA Leu Tyr Met Ala Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val 285 290 295 300	915
ATT CTC CCG CTG ATA TAT TTC ATA GTC GTA CGA AAG AAC CCT TTC CGA Ile Leu Pro Leu Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg 305 310 315	963
TTT GCC ATG GGA ATG GCC CAG GCT CTC CTG ACA GCT CTC ATG ATC TCT Phe Ala Met Gly Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser 320 325 330	1011
TCC AGT TCA GCA ACA CTG CCT GTC ACC TTC CGC TGT GCT GAA GAA AAT Ser Ser Ser Ala Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn 335 340 345	1059
AAC CAG GTG GAC AAG AGG ATC ACT CGA TTC GTG TTA CCC GTT GGT GCA Asn Gln Val Asp Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala 350 355 360	1107
ACA ATC AAC ATG GAT GGG ACC GCG CTC TAT GAA GCA GTG GCA GCG GTG Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Ala Val 365 370 375 380	1155
TTT ATT GCA CAG TTG AAT GAC CTG GAC TTG GGC ATT GGG CAG ATC ATC Phe Ile Ala Gln Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile 385 390 395	1203
ACC ATC AGT ATC ACG GCC ACA TCT GCC AGC ATC GGA GCT GCT GGC GTG Thr Ile Ser Ile Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val 400 405 410	1251

Figure 4 (cont'd.)

CCC CAG GCT GGC CTG GTG ACC ATG GTG ATT GTG CTG AGT GCC GTG GGC Pro Gln Ala Gly Leu Val Thr Met Val Ile Val Leu Ser Ala Val Gly 415 420 425	1299
CTG CCC GCC GAG GAT GTC ACC CTG ATC ATT GCT GTC GAC TGG CTC CTG Leu Pro Ala Glu Asp Val Thr Leu Ile Ile Ala Val Asp Trp Leu Leu 430 435 440	1347
GAC CGG TTC AGG ACC ATG GTC AAC GTC CTT GGT GAT GCT TTT GGG ACG Asp Arg Phe Arg Thr Met Val Asn Val Leu Gly Asp Ala Phe Gly Thr 445 450 455 460	1395
GGC ATT GTG GAA AAG CTC TCC AAG AAG GAG CTG GAG CAG ATG GAT GTT Gly Ile Val Glu Lys Leu Ser Lys Lys Glu Leu Glu Gln Met Asp Val 465 470 475	1443
TCA TCT GAA GTC AAC ATT GTG AAT CCC TTT GCC TTG GAA TCC ACA ATC Ser Ser Glu Val Asn Ile Val Asn Pro Phe Ala Leu Glu Ser Thr Ile 480 485 490	1491
CTT GAC AAC GAA GAC TCA GAC ACC AAG AAG TCT TAT GTC AAT GGA GGC Leu Asp Asn Glu Asp Ser Asp Thr Lys Lys Ser Tyr Val Asn Gly Gly 495 500 505	1539
TTT GCA GTA GAC AAG TCT GAC ACC ATC TCA TTC ACC CAG ACC TCA CAG Phe Ala Val Asp Lys Ser Asp Thr Ile Ser Phe Thr Gln Thr Ser Gln 510 515 520	1587
TTC TAGGGCCCCT GGCTGCAGAT GACTGGAAAC AAGGAAGGAC ATTTCTGTGAG Phe 525	1640
AGTCATCTCA AACACGGCTT AAGGAAAAGA GAAA	1674

ASCT1 MEKSNETNGYLD SAQAGPAAGPGAPGTAAGRARRCARFLRRQALVLL - TVSCVLAGAGLGAALR - GL  
GLAST1 MTKSNGEPRMGSRMTFRFOOGVRKRTLLAKKKVONITKEOVKSYLFRNAFVLL - TVSAVIVGTILGFALRPY -  
GLT1 MASTEGANNMPKQVEVRMHOSHLSSEEPKHRNLGMRMCDKLGKNLLLSLTVFCVILGAVCGGLRLAA  
EAAC1 MGKPARKGCDOSKRFLKNNWLLS - TVVAIVLGIVIGVLRREYS

66 SL SRTQVTYLAFPGEMLRMLRMILPLVVC SLVSGAASLDASCLGR LGGIRVAYFGL - TILSASALAVAFI  
72 KMSYREVVKYFSFPGELMRMLQMLVLPLIISSLVTGMAALOSKASGKMGM - RAVVYVMTITIIAVVIGIIVII  
69 PIHPDVVMLIAFPGLMRMLKMLILPLIISSLITGLSGLOAKASGR LGT - RAMVYVMTITIIAVLGVILVLA  
43 NLSTLQKFYFAFPGLMRMLKLVILPLIVSSMITGVVALDSNVSGKIGL - RAVLVYVFTTIIAVILGIVLVVS

139 IKPGSGAQTLOSSDLGLEDSGPPVPKETVDSFLDLARNLFP SNLVAAFRTYATDYKVV - - - - - TQNSSS  
145 IHPGKGT - KENMYREGKIVOVTA - - - - - ADAFLDLIRNMFPPNLVEACFKQFKTSYEKRSFKVPIOANETLLG  
142 IHPGNPKLTKQLGPGKKNDDEVSS - - - - - LDAFLDLIRNLFPENLVOACFOQIOTVTKKVLVAPPS - EEANTTK  
116 IKPGVTQKVDEIDRTGSTPEVST - - - - - VDAMLDLIRNMFPEENLVOACFOQYKTTREEV - - - - - TASOOTGKNGTE

205 GNVTHEKIPIGTEI - - - - - EGMNLLGLVLFALVLGVALKKLGSEGEDLIRFENSLEATMVLVSW  
212 AVINNVSEAMETLTRIREEMVPVPGSVN - GVNALGLVVPSCMCFGVIGNNKEOGALREFFOSLEAIVRLVAV  
209 AVISLLNETMNEAPEETKIVIKKGLEFKDGMNVLGLIGFFIAFGIAMGKMGVAGQADGGVLQHSERDCHEVSDH  
182 ESVTAVMTTAVSENRTKEYRVVGLYS - - - - - DGINVLGLIVFCLVFGLVIGKMGEGGOILVDFENALSOATWKIVOI

265 IMWVYVVGIMFLVGSKYVEMKQIIVLVTS LGKYIFASLGHVTHGGIVLPLIYFVTRKNPREFLLGLLAPFAT  
285 IMWYAPLGLILFLIAGKILEMEOMGVIGGOLAMVTVTVIVGLIHAVIVLPLLYFLVTRKNPWFIFIGLLLOALIT  
283 DHVVPAGIACLICGKIIA KOLEVVAROLGMYMITVIVGLIHHGIFLPLIYFVTRKNPFSFFAGIFOAWIT  
254 IMCYMPLGLILFLIAGKILEVEDWEIF - RKLG LYMVTVLSGLAHSIVILPLIYFIVVRKNPREFAMGMTQALLT

339 AFATCSSSATLPSPMMKCI EENNGVOKRISRIFLPIGATVNMGGAAIFOCVAAVFIAQLNNIELNAGOIITILVT  
359 ALGTSSSSATLPITFKCLEENNGVDKRITRFVLPVGATINMDGTALYEALAAIFIAQVNNFOLNFGQIITISIT  
357 ALGTASSAGTLPVTFRCLEDNLTKRVTRFVLPVGATINMDGTALYEAVAAIFIAQMNNGVILOGGOIVTVSLT  
327 ALMTSSSSATLPVTFRCAEENNRVDKRITRFVLPVGATINMDGTALYEAVAAVFIQALNDOMLSIGOIITISVT

413 ATASSVGAAGVPAAGVLTIAITLEAIGLPTHOLPLILAVDWIVORTTIVNVVEGOALGAGILHHLNOKATKKGE  
433 ATAASIGAAGIPOAGLVMTVIVLTSVGLPTDDITLIIVADWFLDGLRITTNVLGDSLGAGIVEHLSRHELKNRD  
431 ATLASIGAASIPSAGLVTMLLILTAVGLPTEDISLLVAVDWLDFMRITSVNVVVGDSFGAGIVYHLSKSELDITC  
401 ATAASIGAAGVPOAGLVMTVIVLSAVGLPAECVTLTIAVDWLLDFRTVNVNLGDAFGTGIVEKLSKKKELEOMQ

487 QELAEVKVEAIPNCKSEETSPLVTHONPAGPVASAPELESKESVL 532  
507 VEMGNSVIEENEMKKPYQLIAODNEPEKPVADSETKM 543  
505 SQHRMHEDIEMTKTQSVYDOTKNHRESNSNOCVYAAHNSVVIDECKVTLAANGKSADCSVEEEPWKREK 573  
475 VSSEVNIVNPFALLESATLONEDSOTKKSYINGGFAVDKSDTISFTQTSQF 524

Fig. 5

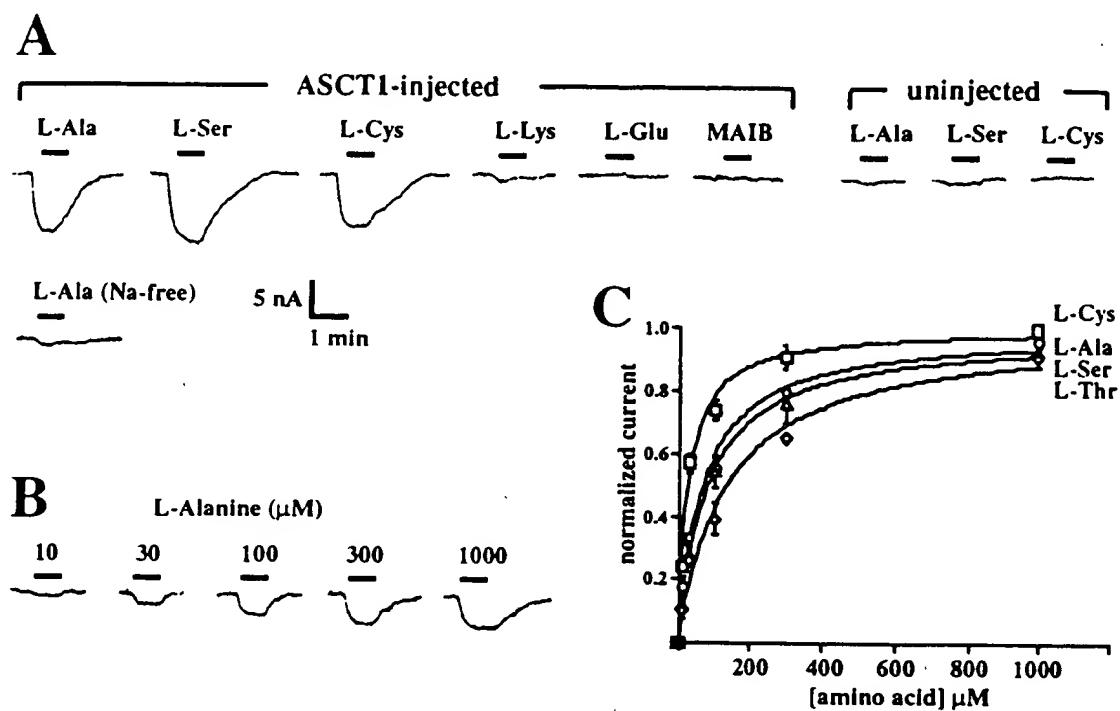


Fig. 6

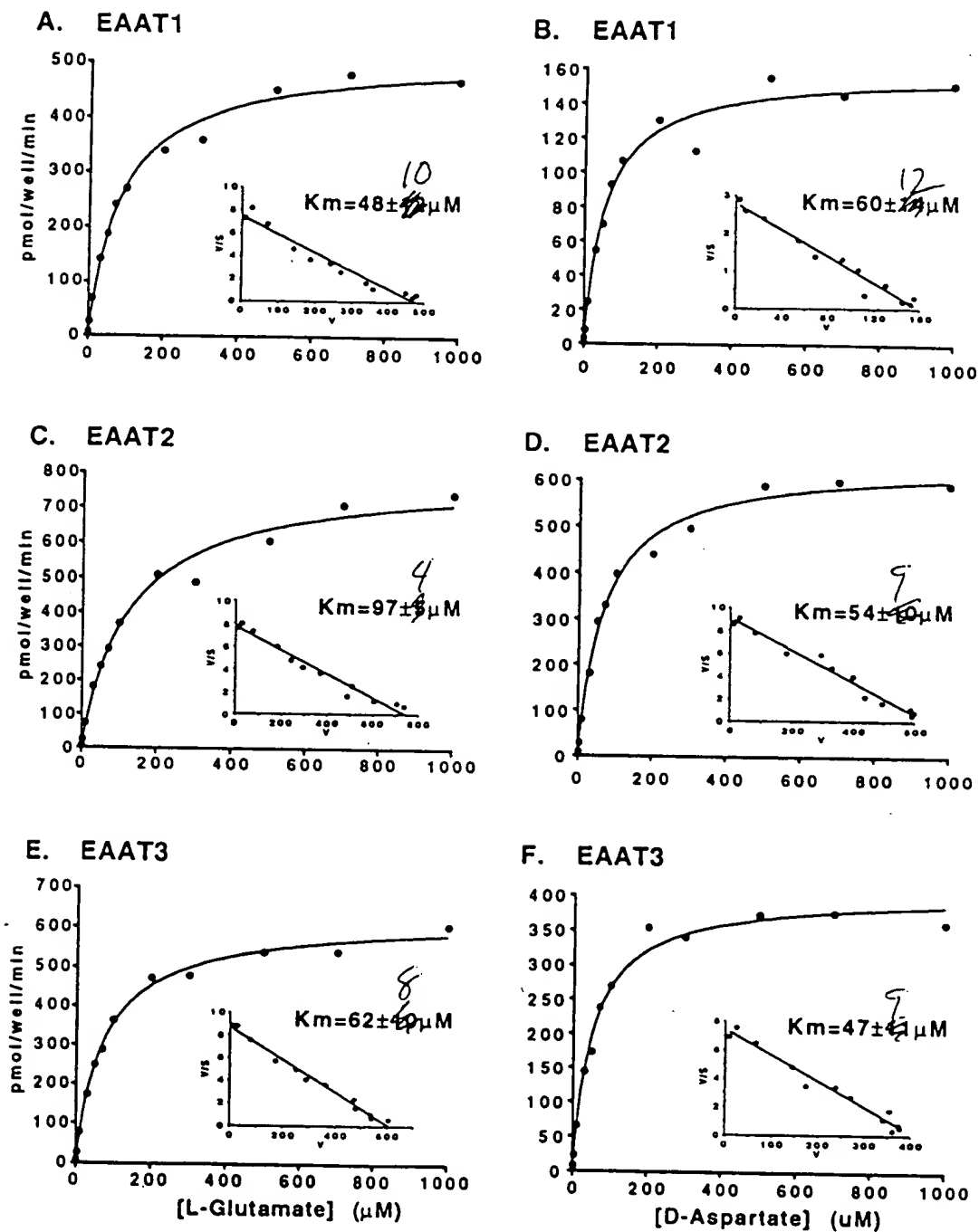
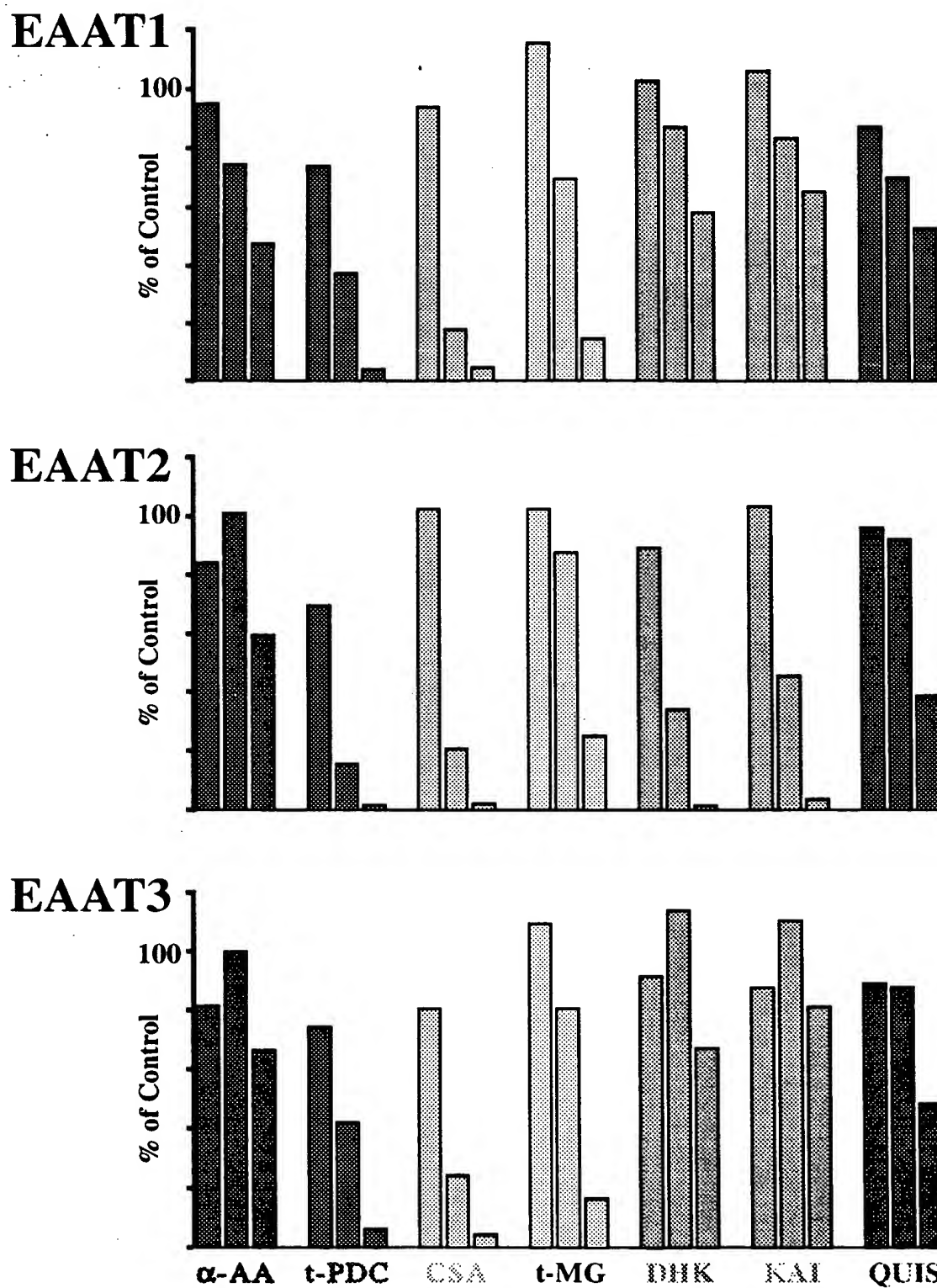


Fig. 7

# Glutamate Transporter Pharmacology



1  $\mu$ M L-Glu with inhibitors at 3  $\mu$ M, 100  $\mu$ M, or 3 mM



Fig. 9

## Distribution of Transporter mRNAs in Human Tissues

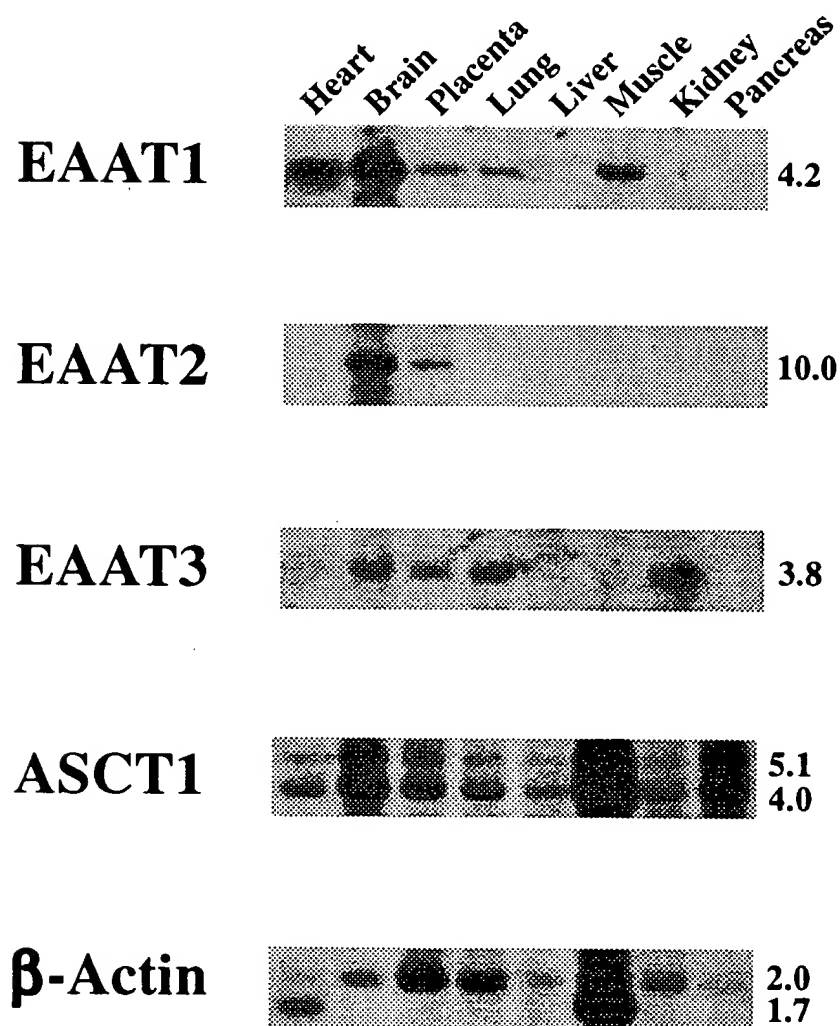
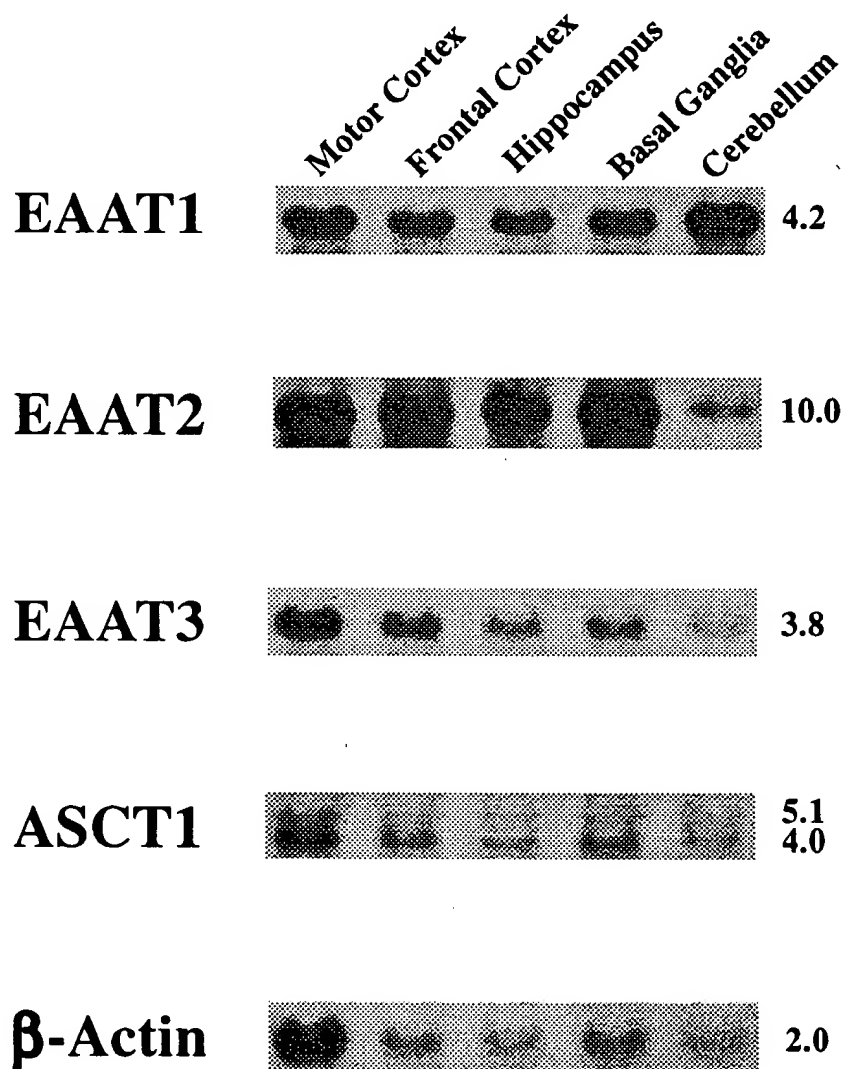


Fig. 10

## Distribution of Transporter mRNAs in Regions of the Human Brain



EAAT1 MTKSNGEEPKMGGRMERFOQGVKRTLLAKKKVQ<sup>N</sup>ITKKDVKSYLEFGNPFVLL...TVTAVIVGTILGFTLRPY.  
EAAT2 MASTEGANNMPKQVEVRMPDHLGSEEPKRRHLGLRLCDKLGKNLLTLTVFGVILGAVCGGLLRLAS  
EAAT3 MGKPAKRGCPSWKRFLKNWVLLS...TVAAVLGITTVLVREHS

72 RMSYREVKYFSFPGELLMRMLQMLVLPLISSLVTGMAALDSKASGKMGMRAVVVYMTTIIAVVIGIIVII  
69 PIHPDVMLIAFPQDILMRMLKMLILPLISSLITGLSGLDAKASGRLGTTRAMVVYMSSTIIAAVLGVILVLA  
44 NLSTLEKFYFAFPGEILMRMLKLIILPLISSLITGVAAALDSNVSGKIGLRAVVVYFCTTIIAVLGVILVVS

146 HPGKGT KENMHREGKIVRVTAADAFLOLIRNMFPNLEACFKQFKTGYEKRSFKVPFIOANETLVGAVINVS  
143 HPGNPKL KQOLGPKMNDDEVSSDAFLOLIRNLFENLVQACFQOIOTVTKKVLVAPPDEEANAATSAEVSLLN  
118 KPGVTQKVGEIAPTGSTPEVSTVDAMLDLIRNMFPENLVQACFOOYKTKREEV...KPPSDPEANMTESFTAM

219 EAMETLTRITEELVPVPGSVN.GVNALGLVVFVSMCFGFVIGNMKEQQAALREFFDSLNEAIRMVLVAVIMWYAPE  
217 ETVTEVPEETKMVKKGLEFKDGMNVLGLIGFFIAFGIAMGKMGOAKLMVDFFNILNEIVMKLVIMMWYSL  
190 TTAISK<sup>N</sup>KTKEYKIVGMYS...DGINVVLGLIVFCLVFGLVIGKMGEGKOILVDFFNALSDATMKIVQITMCYML

292 GILFLIAGKIVEMEDMGVIGGOLAMYTVTVIVGLLIHAVIVLPLLYFLVTRKNPWFVIGGLLOALITALTGTSS  
291 GACLCGKIATAKDLEVVAROLGMYMVTIIGLIHGGIFLPLIYFVVTAKNPFSLFAGIFOAWITALGTSS  
261 GILFLIAGKITEVEDWEIFRKGLGLYMATVLTGLAHSIVILPLIYFIVVRKNPFRFAMGMAOALITALMISS

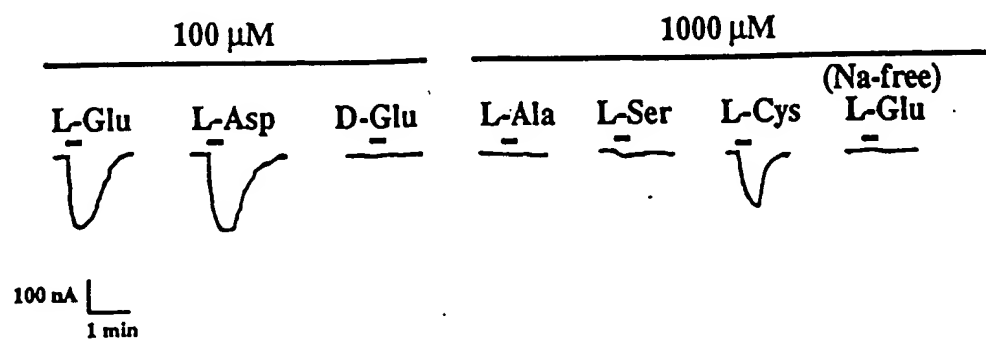
366 SATLPITFKCLEENNGVDKRVTRFVLPVGATINMOGTALYEALAAIFIAQVNNFELNFGOITISITATAASIG  
365 AGTLPVTFRCLEENLGIDKRVTRFVLPVGATINMOGTALYEAVAAIFIAQMNGVVLDDGOITISITATLASV  
334 SATLPVTFRCLEENNOVDKRIITRFVLPVGATINMOGTALYEAAVAFIAQLNDLDLIGOITISITATLASIG

440 AAGIPQAGLVTVIVLTSVGLPTDITLIIAVDWFLDRRTTINVLGDSLGGAGIVEHLSAHELKNROVEMGNSV  
439 AASIP<sup>S</sup>SAGLVTVLIIITAVGLPTDIIISLVAVDWLLDRMRTSVNVVGDSTFGAGIVVHLSKSELOTIDSOHRAVHE  
408 AAGVPOAGLVTVIVLSAVGLPAEDVTLIIAVDWLLDRFRTMVNVLGDAFGTGIVEKLSKKELEOMOVSSSEVNI

514 IEE<sup>N</sup>NEMKKPYQLIAQD<sup>N</sup>ETEKPIDSETKM 542  
513 DIEMTKTOSYDOMKNHRESNSNOCVYAAHNSVIVDECKVTLAANGKSADCSVEEPPWKREK 574  
482 VNPFALESTLDNEDSDTKKSYVNGGFAVOKSDTISFTQTSOF 525

Fig. 11

A



B

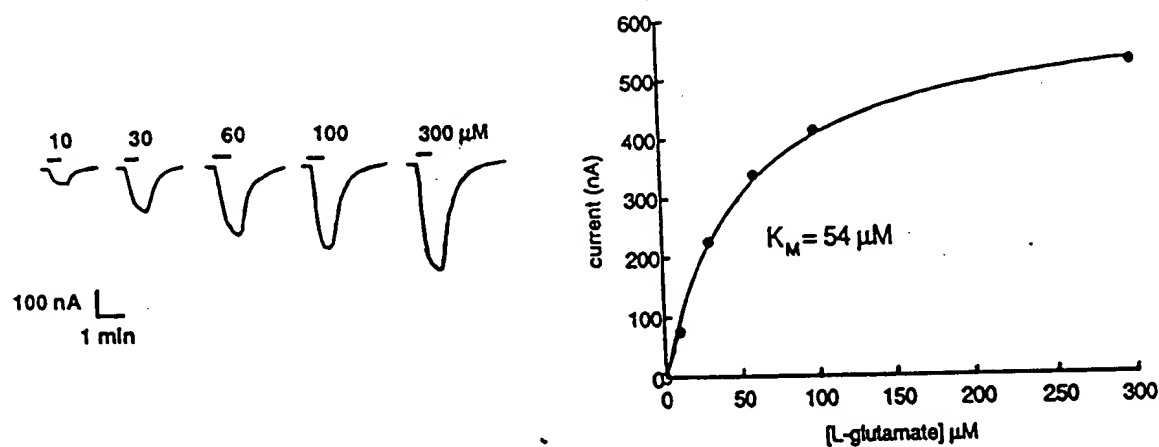


Fig. 12